

# Patricia C Babbitt

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7360547/publications.pdf>

Version: 2024-02-01

121  
papers

11,971  
citations

34016

52  
h-index

28224

105  
g-index

129  
all docs

129  
docs citations

129  
times ranked

15561  
citing authors

#	ARTICLE	IF	CITATIONS
1	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
2	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291
3	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
4	Annotation Error in Public Databases: Misannotation of Molecular Function in Enzyme Superfamilies. <i>PLoS Computational Biology</i> , 2009, 5, e1000605.	1.5	587
5	Divergent Evolution of Enzymatic Function: Mechanistically Diverse Superfamilies and Functionally Distinct Suprafamilies. <i>Annual Review of Biochemistry</i> , 2001, 70, 209-246.	5.0	502
6	Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. <i>PLoS ONE</i> , 2009, 4, e4345.	1.1	385
7	The Enolase Superfamily: A General Strategy for Enzyme-Catalyzed Abstraction of the $\hat{\pm}$ -Protons of Carboxylic Acidsâ€”. <i>Biochemistry</i> , 1996, 35, 16489-16501.	1.2	331
8	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
9	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
10	Understanding Enzyme Superfamilies. <i>Journal of Biological Chemistry</i> , 1997, 272, 30591-30594.	1.6	253
11	BayGenomics: a resource of insertional mutations in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2003, 31, 278-281.	6.5	220
12	The Structureâ€”Function Linkage Database. <i>Nucleic Acids Research</i> , 2014, 42, D521-D530.	6.5	210
13	Evolution of enzyme superfamilies. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 492-497.	2.8	209
14	Divergent evolution in the enolase superfamily: the interplay of mechanism and specificity. <i>Archives of Biochemistry and Biophysics</i> , 2005, 433, 59-70.	1.4	194
15	Evolutionary Potential of ( $\hat{2}/\hat{\pm}$ )8-Barrels: A Functional Promiscuity Produced by Single Substitutions in the Enolase Superfamilyâ€”. <i>Biochemistry</i> , 2003, 42, 8387-8393.	1.2	171
16	The Enzyme Function Initiative. <i>Biochemistry</i> , 2011, 50, 9950-9962.	1.2	169
17	Leveraging Enzyme Structureâ€”Function Relationships for Functional Inference and Experimental Design:â€” The Structureâ€”Function Linkage Database. <i>Biochemistry</i> , 2006, 45, 2545-2555.	1.2	157
18	Divergence of Function in the Thioredoxin Fold Suprafamily: A Evidence for Evolution of Peroxiredoxins from a Thioredoxin-like Ancestorâ€”. <i>Biochemistry</i> , 2004, 43, 13981-13995.	1.2	141

#	ARTICLE	IF	CITATIONS
19	Can sequence determine function?. <i>Genome Biology</i> , 2000, 1, reviews0005.1.	13.9	132
20	Enzyme (re)design: lessons from natural evolution and computation. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 10-18.	2.8	126
21	Glutathione Transferases Are Structural and Functional Outliers in the Thioredoxin Fold. <i>Biochemistry</i> , 2009, 48, 11108-11116.	1.2	125
22	Discovery of new enzymes and metabolic pathways by using structure and genome context. <i>Nature</i> , 2013, 502, 698-702.	13.7	124
23	Unexpected Divergence of Enzyme Function and Sequence: A N-Acylamino Acid Racemase Iso-Succinylbenzoate Synthase. <i>Biochemistry</i> , 1999, 38, 4252-4258.	1.2	118
24	Divergent Evolution in Enolase Superfamily: Strategies for Assigning Functions. <i>Journal of Biological Chemistry</i> , 2012, 287, 29-34.	1.6	118
25	An Atlas of the Thioredoxin Fold Class Reveals the Complexity of Function-Enabling Adaptations. <i>PLoS Computational Biology</i> , 2009, 5, e1000541.	1.5	114
26	Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9549-E9558.	3.3	111
27	Mechanistically diverse enzyme superfamilies: the importance of chemistry in the evolution of catalysis. <i>Current Opinion in Chemical Biology</i> , 1998, 2, 607-612.	2.8	107
28	Biases in the Experimental Annotations of Protein Function and Their Effect on Our Understanding of Protein Function Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003063.	1.5	103
29	Differential use of protease families for invasion by schistosome cercariae. <i>Biochimie</i> , 2008, 90, 345-358.	1.3	100
30	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a Plug and Play Domain. <i>Methods in Enzymology</i> , 2018, 606, 1-71.	0.4	99
31	Prediction and assignment of function for a divergent N-succinyl amino acid racemase. <i>Nature Chemical Biology</i> , 2007, 3, 486-491.	3.9	98
32	The global cysteine peptidase landscape in parasites. <i>Trends in Parasitology</i> , 2009, 25, 573-581.	1.5	88
33	Structure-guided discovery of the metabolite carboxy-SAM that modulates tRNA function. <i>Nature</i> , 2013, 498, 123-126.	13.7	84
34	Evidence That <i>pcpA</i> Encodes 2,6-Dichlorohydroquinone Dioxygenase, the Ring Cleavage Enzyme Required for Pentachlorophenol Degradation in <i>Sphingomonas chlorophenolica</i> Strain ATCC 39723. <i>Biochemistry</i> , 1999, 38, 7659-7669.	1.2	81
35	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. <i>ELife</i> , 2014, 3, .	2.8	81
36	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. <i>PLoS Biology</i> , 2014, 12, e1001843.	2.6	79

#	ARTICLE	IF	CITATIONS
37	Prediction of function for the polyprenyl transferase subgroup in the isoprenoid synthase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1196-202.	3.3	75
38	Automated discovery of 3D motifs for protein function annotation. <i>Bioinformatics</i> , 2006, 22, 723-730.	1.8	73
39	Insights into the Mechanism of Catalysis by the P <sup>α</sup> C Bond-Cleaving Enzyme Phosphonoacetaldehyde Hydrolase Derived from Gene Sequence Analysis and Mutagenesis. <i>Biochemistry</i> , 1998, 37, 9305-9315.	1.2	71
40	Definitions of enzyme function for the structural genomics era. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 230-237.	2.8	71
41	structureViz: linking Cytoscape and UCSF Chimera. <i>Bioinformatics</i> , 2007, 23, 2345-2347.	1.8	71
42	3-Carboxy-cis,cis-muconate lactonizing enzyme from <i>Pseudomonas putida</i> is homologous to the class II fumarase family: a new reaction in the evolution of a mechanistic motif. <i>Biochemistry</i> , 1992, 31, 9768-9776.	1.2	68
43	On the origins and functions of the enzymes of the 4-chlorobenzoate to 4-hydroxybenzoate converting pathway. <i>Biodegradation</i> , 1994, 5, 259-276.	1.5	68
44	Evolution of Structure and Function in the o-Succinylbenzoate Synthase/N-Acylamino Acid Racemase Family of the Enolase Superfamily. <i>Journal of Molecular Biology</i> , 2006, 360, 228-250.	2.0	65
45	Functional Assignment of the 20 S Proteasome from <i>Trypanosoma brucei</i> Using Mass Spectrometry and New Bioinformatics Approaches. <i>Journal of Biological Chemistry</i> , 2001, 276, 28327-28339.	1.6	64
46	A gold standard set of mechanistically diverse enzyme superfamilies. <i>Genome Biology</i> , 2006, 7, R8.	13.9	62
47	Cloning and Functional Characterization of a Rat Renal Organic Cation Transporter Isoform (rOCT1A). <i>Journal of Biological Chemistry</i> , 1997, 272, 16548-16554.	1.6	58
48	Evolution of Function in the "Two Dinucleotide Binding Domains" Flavoproteins. <i>PLoS Computational Biology</i> , 2007, 3, e121.	1.5	58
49	Evolutionary constraints on structural similarity in orthologs and paralogs. <i>Protein Science</i> , 2009, 18, 1306-1315.	3.1	58
50	Revealing Unexplored Sequence-Function Space Using Sequence Similarity Networks. <i>Biochemistry</i> , 2018, 57, 4651-4662.	1.2	58
51	New Insights about Enzyme Evolution from Large Scale Studies of Sequence and Structure Relationships. <i>Journal of Biological Chemistry</i> , 2014, 289, 30221-30228.	1.6	57
52	[FeFe]-Hydrogenase Maturation: Insights into the Role HydE Plays in Dithiomethylamine Biosynthesis. <i>Biochemistry</i> , 2015, 54, 1807-1818.	1.2	57
53	Homology models guide discovery of diverse enzyme specificities among dipeptide epimerases in the enolase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4122-4127.	3.3	56
54	Redesigning Enzymes Based on Adaptive Evolution for Optimal Function in Synthetic Metabolic Pathways. <i>Chemistry and Biology</i> , 2008, 15, 607-618.	6.2	53

#	ARTICLE	IF	CITATIONS
55	Discovery of a Dipeptide Epimerase Enzymatic Function Guided by Homology Modeling and Virtual Screening. <i>Structure</i> , 2008, 16, 1668-1677.	1.6	52
56	Mutations in PNKD causing paroxysmal dyskinesia alters protein cleavage and stability. <i>Human Molecular Genetics</i> , 2011, 20, 2322-2332.	1.4	52
57	Superfamily active site templates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 962-976.	1.5	49
58	Molecular Diversity of Terpene Synthases in the Liverwort <i>Marchantia polymorpha</i> . <i>Plant Cell</i> , 2016, 28, tpc.00062.2016.	3.1	48
59	Parallel molecular mechanisms for enzyme temperature adaptation. <i>Science</i> , 2021, 371, .	6.0	48
60	Comparisons of creatine kinase primary structures. <i>The Protein Journal</i> , 1986, 5, 1-14.	1.1	45
61	Inference of Functional Properties from Large-scale Analysis of Enzyme Superfamilies. <i>Journal of Biological Chemistry</i> , 2012, 287, 35-42.	1.6	45
62	SmCL3, a Gastrodermal Cysteine Protease of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e449.	1.3	45
63	The evolution of function in strictosidine synthase-like proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3082-3098.	1.5	43
64	Pythoscape: a framework for generation of large protein similarity networks. <i>Bioinformatics</i> , 2012, 28, 2845-2846.	1.8	42
65	Removal of a Proteolytic Activity Associated with Aggregates Formed from Expression of Creatine Kinase in <i>Escherichia coli</i> Leads to Improved Recovery of Active Enzyme. <i>Nature Biotechnology</i> , 1990, 8, 945-949.	9.4	40
66	Toward mechanistic classification of enzyme functions. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 435-442.	2.8	40
67	A global view of structure-function relationships in the tautomerase superfamily. <i>Journal of Biological Chemistry</i> , 2018, 293, 2342-2357.	1.6	39
68	New functions from old scaffolds: How nature reengineers enzymes for new functions. <i>Advances in Protein Chemistry</i> , 2001, 55, 1-28.	4.4	36
69	Evolution of Enzymatic Activities in the Enolase Superfamily: Stereochemically Distinct Mechanisms in Two Families of <i>cis</i> - <i>cis</i> -Muconate Lactonizing Enzymes. <i>Biochemistry</i> , 2009, 48, 1445-1453.	1.2	36
70	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. <i>Bioinformatics</i> , 2011, 27, 326-333.	1.8	36
71	Evolution of Enzymatic Activities in the Enolase Superfamily: Crystal Structure of (D)-Glucarate Dehydratase from <i>Pseudomonas putida</i> . <i>Biochemistry</i> , 1998, 37, 14358-14368.	1.2	35
72	A Mapping of Drug Space from the Viewpoint of Small Molecule Metabolism. <i>PLoS Computational Biology</i> , 2009, 5, e1000474.	1.5	34

#	ARTICLE	IF	CITATIONS
73	Quantitative Comparison of Catalytic Mechanisms and Overall Reactions in Converгентly Evolved Enzymes: Implications for Classification of Enzyme Function. PLoS Computational Biology, 2010, 6, e1000700.	1.5	33
74	Barrels in pieces? , 2001, 8, 5-7.		29
75	Reengineering the glutathione S-transferase scaffold: A rational design strategy pays off. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10298-10300.	3.3	27
76	Covalent Docking Predicts Substrates for Haloalkanoate Dehalogenase Superfamily Phosphatases. Biochemistry, 2015, 54, 528-537.	1.2	26
77	At the Periphery of the Amidohydrolase Superfamily: Bh0493 from <i>Bacillus halodurans</i> Catalyzes the Isomerization of <i>d</i> -Galacturonate to <i>d</i> -Tagaturonate. Biochemistry, 2008, 47, 1194-1206.	1.2	25
78	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. Journal of Structural and Functional Genomics, 2009, 10, 107-125.	1.2	25
79	Mechanisms of Protein Evolution and their Application to Protein Engineering. Advances in Enzymology and Related Areas of Molecular Biology, 2010, 75, 193-239.	1.3	25
80	Consequences of domain insertion on sequence-structure divergence in a superfold. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3381-7.	3.3	25
81	Structural Diversity within the Mononuclear and Binuclear Active Sites of N-Acetyl-d-glucosamine-6-phosphate Deacetylase. Biochemistry, 2007, 46, 7953-7962.	1.2	23
82	Predicting the Functions and Specificity of Triterpenoid Synthases: A Mechanism-Based Multi-intermediate Docking Approach. PLoS Computational Biology, 2014, 10, e1003874.	1.5	23
83	Determinants of the CmoB carboxymethyl transferase utilized for selective tRNA wobble modification. Nucleic Acids Research, 2015, 43, 4602-4613.	6.5	23
84	A comparative study of human muscle and brain creatine kinases expressed in Escherichia coli. The Protein Journal, 2000, 19, 59-66.	1.1	22
85	Topological variation in the evolution of new reactions in functionally diverse enzyme superfamilies. Current Opinion in Structural Biology, 2011, 21, 391-397.	2.6	22
86	Evolutionarily Conserved Substrate Substructures for Automated Annotation of Enzyme Superfamilies. PLoS Computational Biology, 2008, 4, e1000142.	1.5	21
87	An Atlas of Peroxiredoxins Created Using an Active Site Profile-Based Approach to Functionally Relevant Clustering of Proteins. PLoS Computational Biology, 2017, 13, e1005284.	1.5	19
88	Biophysical studies support a predicted superhelical structure with armadillo repeats for Ricin. Protein Science, 2009, 18, 1139-1145.	3.1	16
89	A semiautomated approach to gene discovery through expressed sequence tag data mining: Discovery of new human transporter genes. AAPS PharmSci, 2003, 5, 1-18.	1.3	15
90	Annotating Enzymes of Uncertain Function: The Deacylation of <i>d</i> -Amino Acids by Members of the Amidohydrolase Superfamily. Biochemistry, 2009, 48, 6469-6481.	1.2	15

#	ARTICLE	IF	CITATIONS
91	The principal islet of the coho salmon ( <i>Oncorhynchus kisutch</i> ) contains the BB isoenzyme of creatine kinase. <i>The Protein Journal</i> , 1992, 11, 489-494.	1.1	14
92	Mechanistic and Bioinformatic Investigation of a Conserved Active Site Helix in $\beta$ -Isopropylmalate Synthase from <i>Mycobacterium tuberculosis</i> , a Member of the DRE-TIM Metallolyase Superfamily. <i>Biochemistry</i> , 2014, 53, 2915-2925.	1.2	14
93	Comparison of topological clustering within protein networks using edge metrics that evaluate full sequence, full structure, and active site microenvironment similarity. <i>Protein Science</i> , 2015, 24, 1423-1439.	3.1	14
94	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 111-132.	0.4	14
95	Representing structure-function relationships in mechanistically diverse enzyme superfamilies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 358-69.	0.7	14
96	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	1.5	13
97	An approach to functionally relevant clustering of the protein universe: Active site profile-based clustering of protein structures and sequences. <i>Protein Science</i> , 2017, 26, 677-699.	3.1	13
98	Exploring the sequence, function, and evolutionary space of protein superfamilies using sequence similarity networks and phylogenetic reconstructions. <i>Methods in Enzymology</i> , 2019, 620, 315-347.	0.4	13
99	Effusion: prediction of protein function from sequence similarity networks. <i>Bioinformatics</i> , 2019, 35, 442-451.	1.8	12
100	New computational approaches to understanding molecular protein function. <i>PLoS Computational Biology</i> , 2018, 14, e1005756.	1.5	11
101	REPRESENTING STRUCTURE-FUNCTION RELATIONSHIPS IN MECHANISTICALLY DIVERSE ENZYME SUPERFAMILIES. , 2004, , .		10
102	Kinetic and structural characterization of a cis-3-Chloroacrylic acid dehalogenase homologue in <i>Pseudomonas</i> sp. UW4: A potential step between subgroups in the tautomerase superfamily. <i>Archives of Biochemistry and Biophysics</i> , 2017, 636, 50-56.	1.4	9
103	Integrated Tools for Structural and Sequence Alignment and Analysis. , 1999, , 230-41.		9
104	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	1.4	8
105	3D Motifs. , 2017, , 361-392.		7
106	DASP3: identification of protein sequences belonging to functionally relevant groups. <i>BMC Bioinformatics</i> , 2016, 17, 458.	1.2	6
107	Biocuration in the structure-function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	6
108	Structural, Kinetic, and Mechanistic Analysis of an Asymmetric 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , 2019, 58, 2617-2627.	1.2	6

#	ARTICLE	IF	CITATIONS
109	Structural Basis for the Asymmetry of a 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , 2020, 59, 1592-1603.	1.2	6
110	Using the Structure-Function Linkage Database to Characterize Functional Domains in Enzymes. <i>Current Protocols in Bioinformatics</i> , 2014, 48, 2.10.1-16.	25.8	5
111	A strategy for large-scale comparison of evolutionary- and reaction-based classifications of enzyme function. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	5
112	Active Creatine Kinase Refolded from Inclusion Bodies in <i>Escherichia coli</i> . <i>ACS Symposium Series</i> , 1991, , 153-168.	0.5	3
113	A Global Comparison of the Human and <i>T. brucei</i> Degradomes Gives Insights about Possible Parasite Drug Targets. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1942.	1.3	3
114	Kinetic and Structural Analysis of Two Linkers in the Tautomerase Superfamily: Analysis and Implications. <i>Biochemistry</i> , 2021, 60, 1776-1786.	1.2	3
115	3D Motifs. , 2009, , 187-216.		3
116	Biocuration in the structure-function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	2
117	Evolutionary Reprograming of Protein-Protein Interaction Specificity. <i>Cell</i> , 2015, 163, 535-537.	13.5	1
118	Intersect: identification and visualization of overlaps in database search results. <i>Bioinformatics</i> , 2003, 19, 1997-1999.	1.8	0
119	Session Introduction. , 2004, , .		0
120	The nature of sequence and structure divergence in the Haloalkanoate Dehalogenase SuperFamily (HADSF). <i>FASEB Journal</i> , 2013, 27, 797.2.	0.2	0
121	Introduction to informatics approaches in structural genomics: modeling and representation of function from macromolecular structure. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 319-21.	0.7	0